

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 131976

TO: James Schultz

Location: rem/2d18/2c18

Art Unit: 1635

Wednesday, September 15, 2004 Case Serial Number: 10/018497 From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527



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From:

Schultz, James

Wednesday, September 08, 2004 1:50 PM

, To: Subject: STIC-Biotech/ChemLib Seq Search 10/018,497

Hello,

Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?

Thanks,

Doug Schultz

James Douglas Schultz, PhD AU 1635 (Biotechnology) Patent Examiner United States Patent and Trademark Office (Office) REM 2D18 (Mail) REM 2C18 (571) 272-0763

STAFF USE ONLY Searcher:_ Searcher Phone: 2-Date Searcher Picked up: Date Completed: 2//5

Searcher Prep/Rev. Time: Online Time:

Type of Search
NA Sequence: #
AA Sequence :#
Structure: #
Bibliographic:
Litigation:
Patent Family:
Other:

Vendors and cost where applicable STN:_ DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS:_ SEQUENCE SYSTEM:

WWW/Internet:_

Other(Specify):__

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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REFERENCE AUTHORS TITLE

Unknown. Unclassified. Unknown

i (bases 1 to 26)
Mitsuhashi,M. and Cooper,A.
Method for detecting polynucleotides with immobilized polynucleotide probes identified based on T.sub.m Patent: US 5639612-A 555 17-JUN-1997;

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

KEYWORDS SOURCE ORGANISM	RESULT 1 146576 LOCUS DEFINITION ACCESSION VERSION		C 44	c 43	41 42	40 40	38	36 37	35	iii iii	c 32	ωı	c 29	N	c 27	่งเง	24	2 22	21	20	18	_	0 0 16 16	۰,	13	c 11	10	wα	7	σ ι	4. n	(L)	N L		Result	
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E 1 (bases 1 to 26)
RS Mitsuhashi, M. and Cooper.A.
Method for detecting polynucleotides with immediate probes identified based on T./
NAL Patent: US 653912-A 665 17-JUN-1997;
Location/Qualifiers
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Nieuhashi,M. and Cooper,A.

Method for detecting polynucleotides with
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Patent: US 5639612-A 560 17-JUN-1997;

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Sequence 541 from patent
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Mitsuhashi,M. and Cooper,A.
Method for detecting polynucleotides with immobilized polynucleotide probes identified based on T.sub.m Patent: US 5639612-A 527 17-JUN-1997;
Location/Qualifiers
1. .22
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Mitsuhashi, M. and Cooper, A.
Method for detecting polynucleotides with immobili polynucleotide probes identified based on T. sub.m Patent: US 5639612 A 672 17-JUN-1997;
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Mitsuhashi,M. and Cooper,A.
Method for detecting polynucleotides with
polynucleotide probes identified based on
Patent: US 5639612-A 546 17-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitsuhashi, M. and Cooper, A. Method for detecting polymicleotides with immobilized polymicleotide probes identified based on T.sub.m patent: US 5639612-A 541 17-JUN-1997;
l Similarity
22; Conserv
                                                                                        1 (bases 1 to 22)
Mitsuhashi,M. and Cooper,A.
Method for detecting polynucleotides with
polynucleotide probes identified based on
Patent: US 5639612-A 588 17-JUN-1997;
Location/Qualifiers
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/mol_type="unassigned DNA"
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/mol_type="unassigned
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I46716
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Mitsuhashi,M. and Cooper,A.
Method for detecting polynucleotides with immobilized polynucleotide probes identified based on T.sub.m Patent: US 5639612-A 695 17-JUN-1997;
Location/Qualifiers
       AR434873
Sequence 1296 from patent
AR434873
AR434873.1 GI:40197716
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Mitsuhashi, M. and Cooper, A.

Method for detecting polynucleotides with immobilized polynucleotide probes identified based on T.sub.m Patent: US 5639612-A 697 17-JUN-1997;
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/mol_type="unassigned
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I46598
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Mitsuhashi,M. and Cooper,A.
Method for detecting polynucleotides with
polynucleotide probes identified based on
Patent: US 5639612-A 577 17-JUN-1997;
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1 (bases 1 to 21)

Mitsuhashi,M. and Cooper,A.

Method for detecting polymucleotides with polymucleotide probes identified based on Patent: US 5639612-A 566 17-JUN-1997;
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                      _type="unassigned DNA"
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Pred. No. 2.2e+06;
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Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 1295 02-DEC-2003;
Location/Qualifiers
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Sequence 1295 from patent
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Mitsuhashi,M. and Cooper,A.

Method for detecting polynucleotides with immobili polynucleotide probes identified based on T. sub.m Patent: US 5639612-A 582 17-JUN-1997;
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17	22	1.4	22	N	AAQ47424	Aaq47424
18	22	1.4	22	N	AAQ47501	Aaq47501
19	22	1.4	22	N	AAQ47497	Aaq47497
20	22	1.4	22	N	AAQ47508	Aaq47508
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Aaq47516	Aaq47475	Aaq47401	Aag47414	Aaq47383	Aaq47413	Aaq47419	Abs75771	Abs75769	Aaq47488	Aaq47405	Aaq47462	Aaq47493	Aaq47485	_	Ade12404	Ade12641	Ade11463	Ade10541	Add67828	Adc24558	Adb89211
Rat G pro	Rat G pro	Common G	Human G p	Sense G p	Human G p	Rat G pro	Human PAP	Human PAP	Human G p	G protein	Human G p	Rat G pro	G protein	Human PAP	Human Gia	Human Gia	Human Gia	Minicell	Human bet	Human Gi	Human Gia

ALIGNMENTS

Probe; quantification; human; GTP binding protein; G protein; alpha subunit; specific mRNA; detection; hybridisation; diagnosis; pathophysiology; diaease state; hereditary; cancer; infectious; osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes; Synthetic. Human G protein, Gi-3, primer HUMGIAB 178. 25-MAR-2003 26-JAN-1994 AAQ47436; AAQ47436 standard; cDNA (revised) (first entry) to mRNA; 26 ₽P.

WO9315221-A1.

05-AUG-1993.

29-JAN-1993;

93WO-US000977.

29-JAN-1992; 24-MAR-1992; 12-NOV-1992; 92US-00827208. 92US-00857059. 92US-00974409.

(HITB) HITACHI CHEM CO LTD. (HITB) HITACHI CHEM RES CENT INC.

Akitaya T, Cooper A, Mitsuhashi M;

WPI; 1993-258695/32.

Quantitating messenger RNA in sample - using immobilised-polynucleotide having sequence complementary to sequence unique to the MRNA.

Claim 15 and 38; Page 46; 177pp; English.

The sequences given in AAQ47433-44 are primers which were used in the quantification of human GTP binding protein (G protein)-specific mRNAs. These primers are derived from human and rat G-protein sequences. These primers were used in conjunction with the method of the invention, in PCR, for the detection and quantification of mRNAs in a sample without

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AAQ47441
ID AAQ47441
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                                                                                                                 Claim 15 and 38; Page 46; 177pp; English
                                                                                                                                                                                            Quantitating messenger RNA in having sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe; quantification; human; GTP binding protein; G protein;
alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
pathophysiology; disease state; hereditary; cancer; infectious;
osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabones
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RES CENT INC.
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The sequences given in AAQ47433-44 are primers which were used in the quantification of human GTP binding protein (G protein)-specific mRNAs

Claim 14 and 38; Page 47; 177pp; English.

Quantitating messenger RNA in sample - using immobilised-polynucleotide having sequence complementary to sequence unique to the MRNA.

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RESULT 3
AAQ477449
ID AAQ4
XX AAQ4
AC AAQ4
XX AAQ4
XX AAQ4
XX AAQ4
XX Prob
KW Prob
KW Por,
XX OSt Synt
XX WO93
PD 05-A
XX WO93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                              29-JAN-1992;
24-MAR-1992;
12-NOV-1992;
                                                                                                                                                                                                                                                                                (HITB )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9315221-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathophysiology; disease state; hereditary; cancer; infectious; osteodystrophy; pituitary tumour; acromegaly; melanoma cells; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; quantification; human; GTP binding protein; G protein; alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat G protein, Gi-3, probe RATBPGTP 230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ47449 standard; cDNA to mRNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP; 7 A; 4 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                        WPI; 1993-258695/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-1993
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                                                                                                                                                                                                                                                                                    HITACHI CHEM CO LTD
HITACHI CHEM RES CEI
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                                                                                                                                                                                                                   Cooper A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                           92US-00827208.
92US-00857059.
92US-00974409.
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                                                                                                                                                                                                                      Mitsuhashi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Le
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The sequences given in AAQ47445-51 are probes which were used in the CC quantification of human GTP binding protein (G protein)-specific mRNAs. CC These probes are derived from human and rat G-protein sequences. These CC probes were used in the method of the invention, for the detection and CC quantification of mRNAs in a sample without the need to purify the mRNA CC from cells. The claimed method comprises identifying a polynucleotide cCC sequence unique to the mRNA, and immobilising an oligomer complementary to this sequence to an insoluble support. The sample is then incubated CC with the insoluble support such that the unique sequence will hybridise to the bound oligomer and be immobilised. Non-immobilised components are CC washed from the support and bound RNA is labelled in such a way that the label is incorporated onto the support relative to the amount of mRNA on CC the support. The amount of bound label is then determined. This method CC can be used for the reliable, rapid, simultaneous quantification of CC multiple varieties of mRNA. It may be used for diagnosing and recognition CC multiple various diseases. G proteins are thought to be involved in CC causing various diseases states, eg. hereditary diseases, CC cancer, and infectious diseases. A genetic deficiency of Gs protein is the CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of hereditary osteodystrophy. Pituitary tumours in CC molecular basis of heredita

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525 26;

Query Match Best Local Similarity

ilarity 100.0%; Conservative

0,

Score 26; Pred. No. Mismatches

DB 2; I 0 Other;

0 Length Indels

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Gaps

0

Sequence

26

ВP;

7 A;

4 C; 9 G; 6 T; 0 U;

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PROSERVE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; quantification; human; GTP binding protein; G protein; alpha subunit; specific mRNA; detection; hybridisation; diagnosis; pathophysiology; disease state; hereditary; cancer; infectious; osteodystrophy; pituitary tumour; acromegaly; melanomer cells; diabetes;
Quantitating messenger RNA in sample - using immobilised-polynucleotide
                                                                                WPI; 1993-258695/32.
                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1992;
24-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
26-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ47456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ47456 standard;
                                                                                                                                                            Akitaya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATGTTCTTCGGACGAGAGTGAAGAC 26
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HITACHI CHEM RES CENT INC
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                                                                                                                                                            Cooper A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                               92US-00827208.
92US-00857059.
92US-00974409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gi-3, probe RATBPGTP 231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93WO-US000977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA to mRNA; 26 BP
                                                                                                                                                                 Mitsuhashi M;
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WPI; 2003-711671/67

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB89210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                             05-JUN-2001; 2001US-0295566P.
25-FEB-2002; 2002US-0359843P.
                                                                                                                                                                                                        28-MAY-2002; 2002US-00157305
                                                                                                                                                                                                                                        04-SEP-2003.
                                                                                                                                                                                                                                                                    US2003166099-A1
                                                                                                                                                                                                                                                                                                                                                                          Human Gialpha construct PCR primer #1
                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB89210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB89210 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14 and 38; Page 47; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      having sequence complementary to sequence unique to the MRNA
                                          Sabbadini RA, Surber MW,
                                                                                                                 (SABB/)
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                             cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             921 TGCCAGTTTGAAGATCTGAACAGAAG
                                                                    ) SABBADINI R A.
) SURBER M W.
) BERKLEY N.
) SEGALL A M.
) KLEPPER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGCCAGTTTGAAGATCTGAACCGAAG
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                                                                                                                                                                                                                                                                                                                                           gene therapy; minicell; membrane protein; cancer; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 C; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                           Berkley N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.4; D
Pred. No. 1.6e
0; Mismatches
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                                           Segall AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                           Klepper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                     ss; minicell; episomal expression construct; cancer; asthma; allergy; inflammation; rheumatcoid arthritis; diabetes; Alzheimer's disease; Parkinson's disease; HIV; bacterial infection; hepatitis; myocardial ischaemia; human; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New minicell comprising a mearcheabacterial protein or composition for treating or
                                                                                                                      24-MAY-2001;
                                                                                                                                                     28-MAY-2002; 2002US-00157215.
                                                                                                                                                                                                                       US2003190749-A1
                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        Human Gi alpha cDNA PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC24557 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for preparing a composition for treating or preventing cancer. The present sequence is PCR primer used in the construction of a DNA
                                                                                      24-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
     SURBER M W.
SABBADINI R
SEGALL A M.
BERKLEY N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 89. 
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCTGCACGTTGAGCGCCGAAGACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCTGCACCGTGAGCGCCGAGGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a human gene (or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              construct used
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                                                                                   2001US-0293566P.
2002US-0359843P.
2002US-00154951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to a new minicell comprising a membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a membrane protein consisting of eukaryotic, or organellar protein, useful for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to test the minicell of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.2; D
Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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cc where induction or repression of the gene regulates the copy number of an episomal expression construct and/or causes or enhances the production of construct and/or causes or enhances the copy number of an episomal expression construct and/or causes or enhances minicell production. Also disclosed are compositions causes or enhances minicell production. Also disclosed are compositions can methods for preparing the minicells (or a soluble and/or secreted communicatin, or antibodies and/or antibody derivatives that recognise an antibodies and/or antibody derivatives that recognise an composition and protein, a method of transferring camendrane protein from a minicell membrane to a biological membrane, a method of transferring camendrane protein from a minicell membrane to a biological membrane, a perifically bound by a binding moiety, a method of detecting an agent that is specifically bound by a binding moiety, a method of in situ imaging of three-dimensional structure of a membrane protein, a method of cidentifying ligand-interacting atoms in a defined three-dimensional structure of a membrane protein, a method of cidentifying parent cell is useful for producing anucleic acid that encodes the above protein, and methods of identifying a mucleic acid that concells for diagnostic and therapeutic applications (e.g. in diagnosing or treating cancer, asthma, allegies, inflammation, relumatoid arthritis, cidentify discovery or for delivery of mucleic acid arthritis.

Cc and agents for drug discovery or for delivery of mucleic acid arthritis.
                                                                           invention. Note: The authors have mixed up the seq id numbers between the disclosure and the sequence listing. This means that several of the sequences cannot be conclusively identified and some of the rest may be
                                                                                                                                                      and agents for drug discovery or for delivery of nucleic acids and other bloactive compounds to cells. The present sequence is a human PCR primer used to construct a recombinant DNA for inclusion in a mini-cell of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New minicell-producing parent cell comprising an expression element a mutation in an endogenous gene, useful for producing achromosomal and anucleate cells for diagnostic or therapeutic purposes and for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surber MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell comprises: an expression element that comprises a gene operably linked to expression sequences that are inducible and/or repressible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a minicell-producing parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sabbadini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 204; 242pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Segall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell. The
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ADD67827
ID ADD6
XX
AC ADD6
AC ADD6
AC Hume
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DT 15-\(\cdot\)
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Mini
KW Mini
KW memb
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                                                                                                                                                                                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 26
Minicell; ds; membrane protein; transmembrane domain; membrane anchoring domain; Type III secretion system; achromosomal cell; anucleate cell; cancer; asthma; allergy; inflammation; rheumatoid arthritis; diabetes; Alzheimer's disease; Parkinson's disease HIV infection; bacterial infection; hepatitis; myocardial ischaemia;
                                                                                                Human beta-2
                                                                                                                                                                                              ADD67827 standard; DNA; 29
                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                       GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
                                                                                               adrenergic receptor/ToxR construct
                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                     1.6%;
                                                                                                                                                                                              ВÞ
                                                                                                                                                                                                                                                                                                                                        Score 24.2; I
Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 29;
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Sequence

29 BP;

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œ C; 13

G 2 T;

0 G,

0 Other;

Synthetic. Homo sapiens. Vibrio cholerae.

US2003194714-A1

05-JUN-2001; 2001US-0295566P. 25-FEB-2002; 2002US-0359843P. 28-MAY-2002; 2002US-00157299

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comprising at least one transmembrane domain or at least one membrane con anchoring domain, and a second polypeptide that is not derived from a curanterial protein and is neither a His tag nor a glutathione-S-curansferase polypeptide, where the polypeptide comprises a binding conicty. Also included is the method of introducing a nucleic acid into a cell, comprising contacting the cell with the minicell cited above. The cell which is selected from a eubacterial minicell, a poroplast, a comprising expression sequences operably linked to an ORF construct comprising expression sequences operably linked to an ORF construct comprising expression sequences operably linked to an ORF construct comprising expression sequences operably linked to an ORF construct is mentioned above or encoding a therapeutic polypeptide is a membrane polypeptide or a construct of the proteins mentioned above or encoding a therapeutic comprises a cellular construct of the proteins mentioned above or encoding a therapeutic comprises a cellular crapsesible. These are induced and/or depressed when the binding moiety displayed by the minicell binds to its target compound. The ORF encodes a polypeptide of a biologically active compound contained within or displayed by the minicell binds to its target compound. The ORF encodes a compression of the cell. The system is a Type III secretion system for transferring a molecule from the interior of a minicell into the coll interior and method are useful in producing actromosomal and anucleate cells for diagnostic and therapeutic applications (e.g. in diagnosting or treating cancer, asthma, allergies, inflammation, rheumatoid arthritis, conditions of the colls and agents for drug discovery or for delivery of nucleic acids and other bloacetive compounds to cells. The present sequence is a minicell constituct incorporating human DNA sequence from a gene of interest.
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                                                                           Query Match
Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a minicell comprising at least one nucleic acid. The minicell displays a binding molety directed to a target compound, where the binding molety is selected from a eukaryotic membrane protein, an archeabacterial membrane protein, an organellar membrane protein, and a fusion protein. The fusion protein comprises a first polypeptide
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New minicell useful for producing achromosomal and anucleate cells for diagnosing or treating e.g. cancer, asthma, allergies, inflammation, diabetes, Alzheimer's disease or HIV, and as research tools and agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-844449/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sabbadini RA, Berkley N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 22; SEQ ID NO 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SURB/) SURBER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SABB/) SABBADINI R A. (BERK/) BERKLEY N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery.
                                     11
_
                       GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
  GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
                                                                                                                                                             29
                                                                                                                                                           вP;
                                                                                Conservative
                                                                                                                                                           σ
                                                                                                                                                           A,
                                                                                            1.6%;
                                                                                                                                                           8 C; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surber MW;
                                                                           0;
                                                                         Score 24.2; I
Pred. No. 1.9e
0; Mismatches
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                                                                                                                                                           2 T; 0 U;
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                                                                                                                                                           0 Other;
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                                                                                                                   Length
                                                                                Indels
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RESULT 8
ADE10540
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ADE11462
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                                                                                                                                                                                                                                                                      Matches
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Best Local (
                                                                                                                                                                                                                                                                               membrane protein from a minicell membrane to a biological membrane for preparing a composition for diagnosing or treating hyperproliferative disorders, e.g. cancer. The present sequence represents a minicell associated DNA expression construct PCR primer.
                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of transferring a membrane protein from a minicell membrane to a biological membrane which comprises contacting a minicell to the biological membrane and allowing the minicell and biological membrane to remain in contact for a period of time sufficient for the transfer to occur. The method is useful for transferring a
                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferring a membrane membrane for diagnosing and biological membrane the transfer to occur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein transfer; minicell membrane; biological membrane; hyperproliferative disorder; cancer; ss; PCR; primer.
                                 Human Gialpha XhoI-ClaI fragment PCR primer #1.
                                                                                                                                                                                                                                                                     Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surber MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2001; 2001US-0295566P.
25-FEB-2002; 2002US-0359843P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-2002; 2002US-00157318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003199089-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minicell associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE10540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE10540 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-852795/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SABB/)
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                                                                                                                                                                                              11
                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SURBER M W.
SABBADINI R A.
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       22; SEQ ID NO 204; 243pp; English.
                                                                                                           standard; DNA; 29
                                                                                                                                                                                      GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
                                                                                                                                                                        GGGCTGCACCGTGAGCGCCGAGGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sabbadini RA;
                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                          (first
                                                                                                                                                                                                                                                                     6 A;
                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA expression construct PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                 1.6%;
                                                                                                                                                                                                                                                                     8 C; 13 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein from a minicell membrane to a biological or treating e.g. cancer by allowing the minicell to remain in contact for a sufficient time for
                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                  Score 24.2;
Pred. No. 1.
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                        29
                                                                                                                                                                                                                                  DB 9;
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                                                                                                                                                                                                                                            Length 29;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                      0;
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Minicell; eukaryotic expression sequence; open reading frame; ORF; eubacterial minicell; poroplast; spheroplast; protoplast;

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RESULT 10
ADE12640
ID ADE127
XX
AC ADE12
XX
XX
ADE12
XX
XX
AC ADE12
XX
XX
DT 29-JA
XX
XX
DT 29-JA
XX
XX
Winic
KW Minic
KW eubac
KW echac
KW achro
                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                       CC from a minicell to a cell, determining the amount of a nucleic acid CC transferred to a cell from a minicell and detecting the expression of an CC expression element in a cell. The minicell comprises an expression of an CC element having eukaryotic expression sequences operably linked to an open CC display a binding group and the binding group displays an epitope of the CC cell. The minicell is a euhacterial minicell, a poroplast, a spheroplast CC antibody or antibody derivative, especially a single-chain antibody, an aptamer or an organic compound. The detectable polypeptide is a CC fluorescent polypeptide. The methods are used in the production of CC diagnostic and therapeutic uses, as well as research tools and agents for drug discovery. The present sequence is a PCR primer used to construct a CC minicell construct of the invention incorporating a human DNA sequence. CC Conclusively identified.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2001;
25-FEB-2002;
24-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the rate of transfer of nucleic acid from a minicell to cell (and vice versa) useful in the production of achromosomal and anucleate cells used for diagnostic and therapeutic applications.
         Minicell; eukaryotic expression sequence; open reading frame; ORF; eubacterial minicell; poroplast; spheroplast; protoplast; achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;
                                                                      Human Gialpha
                                                                                                                                                                ADE12640
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 22; SEQ ID NO 204; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sabbadini RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-2002; 2002US-00157391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003166279-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            achromosomal cell; anucleate cell; drug discovery; ss; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SABB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BERK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                    11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SABBADINI R A. BERKLEY N.
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                         GGGCTGCACCGTGAGCGCCGAGGACAAGG
                                                                                                                                                                                                                                                                                                                                                             BP; 6 A; 8 C; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0293566P.
2002US-0359843P.
2002US-00154951.
                                                                                                    (first entry)
                                                                      XhoI-ClaI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to determining the rate of all to a cell, determining the amount
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berkley
                                                                                                                                                                                                                                                                                                                1.6%;
                                                                                                                                                                DNA;
                                                                                                                                                                  29
                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                          G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 Score 24.2; DB 9; Length 29; Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                      PCR
                                                                      primer
                                                                                                                                                                                                                                          29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transfer
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RESULT 11
ADE12403
ID ADE12
XX ADE12
AC ADE12
XX Z
DT 29-JP
XX Y
Minic
KW eubac
KW eubac
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                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                          CC from a minicell to a cell, determining the amount of a nucleic acid CC transferred to a cell from a minicell and detecting the expression of an CC expression element in a cell. The minicell comprises an expression CC element having eukaryotic expression sequences operably linked to an open CC reading frame (ORP) encoding a detectable polypeptide, the minicells CC display a binding group and the binding group displays an epitope of the CC or a protoplast. The cell is a eukaryotic cell. The binding group is an CC antibody or antibody derivative, especially a single-chain antibody, an aptamer or an organic compound. The detectable polypeptide is a CC fluorescent polypeptide. The methods are used in the production of CC achromosomal and anucleate cells useful for applications such as an CC diagnostic and therapeutic uses, as well as research tools and agents for diagnostic and therapeutic uses, as well as research tools and agents for CC diagnostic and therapeutic uses, as well as research tools and agents for CC minicell construct of the invention incorporating a human DNA sequence. CC Note: The authors have mixed up the SCQ ID numbers between the text and CC conclusively identified.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 26
Minicell; eukaryotic expression sequence; open reading freubacterial minicell; poroplast; spheroplast; protoplast; achromosomal cell; anucleate cell; drug discovery; ss; hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                 Human Gialpha XhoI-ClaI fragment
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying an agent that specifically binds a target compound, especially a membrane protein, comprises contacting a minicell displaying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sabbadini RA, Berkley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2001; 2001US-0293566P
25-FEB-2002; 2002US-0359843P
24-MAY-2002; 2002US-00154951
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                                                                                                      29-JAN-2004
                                                                                                                                                                       ADE12403 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 22; SEQ ID NO 204; 242pp; English.
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(BERK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target compound with a library of compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to determining a minicell to a cell, determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                          11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SABBADINI R
BERKLEY N.
                                                                                                                                                                                                                                                                                                                                            1.6%;
Similarity 89.7%;
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                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                             BP; 6 A; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-00157096.
                                                                                                                                                                         DNA;
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                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                             C; 13
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                                                                                                                                                                                                                                                                                                                            Score 24.2; DB 9;
Pred. No. 1.9e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                             G; 2 T; 0 U;
                                                                    PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the rate of transfer
                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                 0 Other;
                                                                                                                                                                                                                                                                                                                                                            Length 29;
                                     frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of nucleic acid
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                                     ORF;
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Gaps

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ARASULT 12
ARASSO3
ID ARASS
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AC ARASS
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DT 28-JU
DT 28-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc from a minicell to a cell, determining the amount of a nucleic acid cc transferred to a cell from a minicell and detecting the expression of an cc expression element in a cell. The minicell comprises an expression cc element having eukaryotic expression sequences operably linked to an open cc display a binding group and the binding group displays an epitope of the cell. The minicell is a eukaryotic cell. The protoplast. The cell is a eukaryotic cell. The binding group is an epitope of the cc or a protoplast. The cell is a eukaryotic cell. The binding group is an cc antibody or antibody derivative, especially a single-chain antibody, an cell compound. The detectable polypeptide is a cc aptamer or an organic compound. The detectable polypeptide is a cc fluorescent polypeptide. The methods are used in the production of cc diagnostic and anucleate cells useful for applications such as cc diagnostic and therapeutic uses, as well as research tools and agents for construct of the invention incorporating a human DNA sequence. Note: The authors have mixed in the formation between the text and creaming the sequence of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                 Human; G-alpha-i3; G protein; Gi protein; adenylyl cyclase; dopamine; thyrotropin-releasing hormone; somatostatin; signal transduction pathway; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition comprising minicells, useful for preventing, treating or diagnosing cancer, asthma or HIV, or as reagents in drug discovery and functional proteomics, as research tools or in compound
                                                                                                                   Human G-alpha-i3
                                                                                                                                                                   28-JUL-2000 (first entry)
                                                                                                                                                                                                                      AAA15503
                                                                                                                                                                                                                                                                 AAA15503 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the sequence listing such that some of the sequences cannot be conclusively identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to determining the rate of transfer of nucleic acid from a minicell to a cell, determining the amount of a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 22; SEQ ID NO 204; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkley N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2002; 2002US-0359843P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-2002; 2002US-00156811.
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KLEPPER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SABBADINI R A.
                                                                                                                                                                                                                                                                                                                                                                                     GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klepper R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%;
                                                                                                                      PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sabbadini RA;
                                                                                                                 forward primer.
                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24.2; DB 9 Pred. No. 1.9e+04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
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RESULT 13
AAA15504/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the dopamine, thyrotropin-releasing hormone and somatostatin signal transduction pathways. The specification describes a number of antisense oligonucleotides which modulate the expression of G-alpha-i3 and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a PCR primer for the human G-alpha-i3 gene. The protein produced from this gene is a member of the G protein family, and more specifically of the Gi family. The Gi proteins are involved in hormonal inhibition of adenylyl cyclase and the regulation of plasma membrane enzymes. In addition, G-alpha-i3 has been shown to have a role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compounds targeting nucleic acids encoding human G-alpha-I3 useful for treating diseases associated with G-alpha-I3 expression and as prophylaxis to prevent or delay infection, inflammation or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2000.
                                                                                                                                                                                                                     Human; G-alpha-i3; G protein; Gi protein; adenylyl cyclase; dopamine;
thyrotropin-releasing hormone; somatostatin; signal transduction pathway;
                                                                                                                                                                                                                                                          Human G-alpha-i3 gene PCR reverse primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to prevent infection, inflammation and tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999;
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                        Cowsert LM;
                                                (ISIS-) ISIS
                                                                           24-JUN-1999;
                                                                                                    24-JUN-1999;
                                                                                                                            16-MAY-2000.
                                                                                                                                                      US6063626-A
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                         PCR primer; ss.
                                                                                                                                                                                                                                                                                     28-JUL-2000
                                                                                                                                                                                                                                                                                                               AAA15504;
                                                                                                                                                                                                                                                                                                                                        AAA15504 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-375497/32.
                                                                                                                                                                                                                                                                                                                                                                                                                       273 GGACGGCTAAAGATTGACTTTGG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      GGACGGCTAAAGATTGACTTTGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 6 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Col 38; 30pp; English.
                                                  PHARM INC
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHARM INC
                                                                           99US-00339775
                                                                                                     9908-00339775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 23;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                        23
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WPI; 2000-375497/32.

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ARESULT 14
AAQ47412
ID AAQ47412
AC AAQ47
AC AAC46
AC AAC4
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1992;
24-MAR-1992;
12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a PCk primer for the human G-alpha-i3 gene. The protein produced from this gene is a member of the G protein family, and more specifically of the Gi family. The Gi proteins are involved in hormonal inhibition of adenylyl cyclase and the regulation of plasma membrane enzymes. In addition, G-alpha-i3 has been shown to have a role in the dopamine, thyrotropin-releasing hormone and somatostatin signal transduction pathways. The specification describes a number of antisense oligonucleotides which modulate the expression of G-alpha-i3 and can be used to prevent infection, inflammation and tumours
  The sequences given in AAQ47409-20 are primers which were used in the quantification of human GTP binding protein (G protein)-specific mRNAs. These primers were used in conjunction with the method of the invention.
                                                                                                                                                  Quantitating messenger RNA in having sequence complementary
                                                                                                                                                                                                                                                                                                                                 (HITB )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; quantification; human; GTP binding protein; G protein; alpha subunit; specific mRNA; detection; hybridisation; diagnosis; pathophysiology; disease state; hereditary; cancer; infectious; osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ47412 standard; cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compounds targeting nucleic acids encoding human G-alpha-I3 useful for treating diseases associated with G-alpha-I3 expression and as prophylaxis to prevent or delay infection, inflammation or tumor
                                                                                                        Claim.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9315221-A1
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26-JAN-1994
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HITACHI
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                                                                                                      and 38; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTGTTTTAGCTGGCAGTGCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTGTTTTAGCTGGCAGTGCTG 351
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                                                                                                                                                                                                                                                                                Cooper A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                        92US-00827208.
92US-00857059.
92US-00974409.
                                                                                                                                                                                                                                                                                                                                 CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gi-3, primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 7 C; 3
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                                                                                                                                                                                                                                                                                                                                 CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%;
                                                                                                      44;
                                                                                                                                                                                                                                                                                     Mitsuhashi
                                                                                                177pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _0_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G; 3 T; 0
                                                                                                                                                     sample - using immobilised-polynucleotide to sequence unique to the MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMGIAB.
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                                                                                                      English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Lo
3.6e+04;
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ARGSULT 15
AAQ47429
ID AAQ47
XX AAQ47
XX AAQ47
XX AAQ47
XX 25-MA
DT 25-MA
DT 26-JA
XX Probe
KW Probe
KW PCR;
XX PCR;
XX WO931
XX WO931
XX WO931
XX HITB
PR 29-JA
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XX AHITB
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XX HITB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC in PCR, for the detection and quantification of mRNAs in a sample without the need to purify the mRNA from cells. The claimed method comprises condentifying a polynucleotide sequence unique to the mRNA, and comprises commobilising an oligomer complementary to this sequence to an insoluble support. The sample is then incubated with the insoluble support such that the unique sequence will hybridise to the bound oligomer and be compositived. Non-immobilised components are washed from the support and compositive to the support and compositive to the amount of mRNA on the support. The amount of bound label is then determined. This method can be used for the reliable, simultaneous quantification of multiple varieties of mRNA. It may be used for diagnosing and recognition of pathophysiology of various diseases states, eg. hereditary diseases, cancer, and infectious diseases. CC disease states, eg. hereditary diseases, cancer, and infectious diseases. CC agnoteins are thought to be involved in causing various disease states. CC agnoteins are thought to be involved in causing various diseases states. CC agnoteins are thought to be involved in causing various diseases states. CC ontain mutant Gs protein is the molecular basis of hereditary contain mutant Gs proteins are also involved in hassive and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
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Best Local
                                                                                                                                                                                                                                                      29-JAN-1992;
24-MAR-1992;
12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; quantification; human; GTP binding protein; G protein; alpha subunit; specific mRNA; detection; hybridisation; diagnosis; pathophysiology; disease state; hereditary; cancer; infectious; pathophysiology; pituitary tumour; acromegaly; melanoma cells; diabetes;
                                                                                                                                                                                                                                                                                                                                                                05-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
26-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ47429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ47429 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                Akitaya T,
                                                                                                                                                                                                                                                                                                                             29-JAN-1993;
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                                                                                                                                                                                                  (HITB ) HITACHI CHEM CO LTD (HITB ) HITACHI CHEM RES CEI
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                                                                                                                                                                Cooper A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first en
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92US-00857059.
92US-00974409.
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                                                                                                                                                              Mitsuhashi M;
                                                                                                                                                                                                   CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22;
Pred. No.
                                                                      sample - using immobilised-polynucleotide to sequence unique to the MRNA.
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Claim 15 and

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45; 177pp; AAQ47421-32

English.

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Quantitating messenger RNA in having sequence complementary

CC quantification of human GTP binding protein (G protein)-specific mRNAs.
CC These primers were used in conjunction with the method of the invention,
CC in PCR, for the detection and quantification of mRNAs in a sample without
CC the need to purify the mRNA from cells. The claimed method comprises
CC identifying a polynuclectide sequence unique to the mRNA, and
CC immobilising an oligomer complementary to this sequence to an insoluble
CC that the unique sequence will hybridise to the bound oligomer and be
CC immobilised. Non-immobilised components are washed from the support and
CC bound RNA is labelled in such a way that the label is incorporated onto
CC the support relative to the amount of mRNA on the support. The amount of
CC bound label is then determined. This method can be used for the reliable,
CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
CC be used for diagnosing and recognition of pathophysiology of various
CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
CC G proteins are thought to be involved in causing various diseases states.
CC A genetic deficiency of Gs protein is the molecular basis of hereditary
CC osteodystrophy. Pituitary tumours in acromegalic patients have been shown
CC contain mutant Gs proteins are also involved in invasive
CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
CC (Updated on 25-MAR-2003 to correct PN field.) Sequence 22 BP; 5 A; 2 C; 8 G; 7 T; 0 U; 0 Other; 601 TGTTTGATGTAGGTGGCCAAAG 622 0; Indels Length 22; <u>,</u> Gaps <u>,</u>

Query Match 1.4%; Score 22; DB 2; L. Best Local Similarity 100.0%; Pred. No. 6.3e+04; Matches 22; Conservative 0; Mismatches 0;

Search completed: September 14, 2004, 14:07:20 Job time : 625 secs

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TGTTTGATGTAGGTGGCCAAAG

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Result
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Maximum DB
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 30
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Match
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Gapop 10.0 , Gapext 1.0
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1543
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| (cgn2_6/ptodata/2/ina/5A_COMB.seq:*
| (cgn2_6/ptodata/2/ina/6A_COMB.seq:*
| (cgn2_6/ptodata/2/ina/6A_COMB.seq:*
| (cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| (cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
| (cgn2_6/ptodata/2/ina/backfIles1.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-379-078-555
US-08-379-078-656
US-08-379-078-655
US-07-974-409C-178
US-07-974-409C-183
US-07-974-409C-183
US-07-974-409C-231
PCT-US93-00977-231
PCT-US93-00977-231
PCT-US93-00977-231
PCT-US93-00977-231
US-08-379-078-527
US-08-379-078-527
US-08-379-078-527
US-08-379-078-588
US-08-379-078-588
US-08-379-078-589
US-08-379-078-589
US-08-379-078-595
US-08-379-078-697
US-09-394-409C-159
US-07-974-409C-169
US-07-974-409C-260
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178, App
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246, App
547, App
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US-08-379-078-555
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Sequence 189, App	•	Sequence 582, App	•		Sequence 1296, Ap		•	-	•	Sequence 260, App	-	•	-	-	•	Sequence 265, App	•	

ALIGNMENTS

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; MOLECULE TYPE: (
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-379-078-555
                                                                                                                                                                                                                                                        COMPUTER READABLE PORM:
COMPUTER READABLE PORM:
COMPUTER: 1BM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/379,078
FILING DATE:
CLASSIFICATION UMBER: US 07/974,406
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 11TACHI.011CP2
TELEPAN: 714-760-9404
TELEPAN: 714-760-9502
INFORMATION FOR SEQ ID NO: 555:
LEDICHCE CHARACTERISTICS:
LEDICHCE CHARACTERISTICS:
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  Query Match 1.7%; Score 26; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 26; Conservative 0; Mismatches 0; Indels
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APPLICANT: Cooper, Allan
TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
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                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: doub!
TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
ITITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Flo
                                                                                                                                                                                        US-08-379-078-665
                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: US-08-379-078-560
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                                                                                                                                                   Sequence 665, Appl
Patent No. 5639612
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLICAL: GUN
MOLECULE TYPE: GUN
HYPOTHETICAL: NO
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/379.079 FILING DATE: CLASSTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: ILLUSTRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cooper, Allan
TITLE OF INVENTION: Gene Detection System
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APPLICANT: Cooper, Allan
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HT
                                                                                                                                                                                                                                                                                                                     Local Similarity
les 26; Conserv
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                                                                                                                                                                      Application US/08379078
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                                                                                                                                                                                                                                                                                                                        Conservative (
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                                    OLSON AND BEAR
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                   16th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEPHONE: 714-760-9502
INFORMATION FOR SEQ ID NO: 665:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Akitay
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                              APPLICATION NUMBER: US/O:
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Alian
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: USA
COUNTRY: USA
2660
                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                NAME: Altman, Daniel E. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                 ZIP: 92660
                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525 GATGTTCTTCGGACGAGAGTGAAGAC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                       E: Knobbe, Martens, Olson, and Bear 620 Newport Center Dr. Sixteenth Floor
                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Akitaya,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA to mRNA
 NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7%; Score 26; DB 1; Length 26; L00.0%; Pred. No. 3e+02;
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HITACHI.006CP2
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NFORMATION FOR SEQ ID NO:

178:

TELEPHONE:

TELECOMMUNICATION INFORMATION:

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; ANTI-SENSE:
US-07-974-409C-183
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                               Query Match 1.7%; Score 26; DB 4; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                   TELEFAX: 714-760-9502
NFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: HI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 620 Newport
CITY: Newport Beach
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 12-NO
                                                                                                                                                                                                                                                                                     TELEPHONE:
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525 GATGTTCTTCGGACGAGAGTGAAGAC 550
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                                                                                                                                                                                  double
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FOR MEASURING MESSENGER RNA
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100.0%; Pred. No. 3e+02;
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                                                                Length 26;
                                 Indels
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US-07-974-409C-230
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                                                                                                                                                                                                                                    PCT-US93-00977-178
                                                                                                                                                                                             Sequence 178, Application PC/TUS9300977 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HIT
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                           NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cl
HYPOTHETICAL: NO
ANTI-SENSE: NO
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APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mitsuhashi
                                                                          STREET: 620 No. Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Wartens, Olson, and Bear STREET: 620 Newport Center Dr. Sixteenth Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   STATE: CA
COUNTRY: USA
                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                              525 GATGTTCTTCGGACGAGAGTGAAGAC 550
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                                                                                                                                                                                                                                                                                                          1 GATGTTCTTCGGACGAGAGTGAAGAC 26
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                                                                                                         E: Knobbe, Martens, Olson, and Bear 620 Newport Center Dr. Sixteenth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
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                                                                                                                                                                                                                                                                                                                                                                           1.7%; Score 26; DB 4; Length 26; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Masato
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IBM PC compatible

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PCT-US93-00977-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 183, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                       TELEFAX: 714-760-9502
NFORMATION FOR SEQ ID NO:
MOLECULE NO HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                 TOPOLICAL: CD
                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 620 Newport Beach
                                                     STRANDEDNESS: dou
TOPOLOGY: linear
                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                         NAME: Altman, Daniel B. REGISTRATION NUMBER: 34,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLOGY:
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                                                                                   NUCLEIC ACID
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                                     cDNA to mRNA
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                                                                       double
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Pred. No.
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PCT-US93-00977-230
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TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LEUGTH: 26
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GENERAL INFORMATION: METHOD AND REAG
                                                                                                                                          Patent No.
                                                                                                                                            Sequence 672, Application US/08379078 Patent No. 5639612
                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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Best Local Similarity
                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE NO
                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                            APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: Gene Dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 19930:
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                                ADDRESSEE:
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Newport Beach
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                E: KNOBBE, MARTENS, OLSON AND BEAR 620 Newport Center Drive 16th Floor
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ilarity 100.0%;
Conservative (
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                                                              Gene Detection System
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US93/00977
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Pred. No.
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Pred. No.
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3e+02;
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3e+02;
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COUNTRY:

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APPLICALL...

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/974,406

FILING DATE: 12-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: HITACHI.C

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 11700-0404

TELEPHONE: 714-760-0404
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US-08-379-078-672
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/DOCKET NUMBER: MITACHI.006CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .07-974-409C-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
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INFORMATION FOR SEQ ID NO: 672:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
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LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Local Similarity 96.2%;
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STRANDEDNESS: double
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Pred. No. 8.3e+02;
                                                                                                                                                                                              Version #1.25
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; MOLECULE TYPE: (
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-974-409C-231
                                                                                                                           STRANDEDNESS: doub
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-231
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PCT-US93-00977-231
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GENERAL INFORMATION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
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Best Local Similarity 96.2%;
                                                                             Query Match
Best Local S
                                                              Matches
                                                                                                                                                                                                                                                                           TELEFAX: 714-760-9502 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0004
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977 FILING DATE: 19930129 CLASSITICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS
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                                                                            / Match 1.6%; Score 24.4; DB 5; Local Similarity 96.2%; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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TOPOLOGY: li
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                              921 TGCCAGTTTGAAGATCTGAACAGAAG 946
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TGCCAGTTTGAAGATCTGAACCGAAG 26
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                                                              Conservative
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                                                            0; Mismatches
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Pred. No. 8.3e+02
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                                                                                           Length 26;
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RESULT 13 US-09-339-775-2

Sequence 2, Application US/09339775 Patent No. 6063626

APPLICANT: Lex M. Cowsert

INFORMATION:

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NUMBER OF SEQ ID NOS: 47

SEQ ID NO 3

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                             RESULT 15
US-08-379-078-527
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US-09-339-775-3/c
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APPLICANT: Lex M. Cowsert

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-I3 EXPRESSION

FILE REFERENCE: RTS-0069

CURRENT APPLICATION NUMBER: US/09/339,775

CURRENT FILING DATE: 1999-06-24
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Best Local Similarity 100.0%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09339775
Patent No. 6063626
                                                                                                                                                                                                                                             Sequence 527, Application US/08379078
Patent No. 5639612
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION FILE REFERENCE: RTS-0069 CURRENT APPLICATION NUMBER: US/09/339,775 CURRENT FILING DATE: 1999-06-24
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, M
                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                               PPLICANT: Cooper, Allan
ITLE OF INVENTION: Gene Detection System
JMBER OF SEQUENCES: 726
                                                 COUNTRY: U:
ZIP: 92660
                                                                                              CITY: Newport Beach
                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                   329 ATTTGTTTTAGCTGGCAGTGCTG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 GGACGGCTAAAGATTGACTTTGG 295
                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                              23;
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                                                                                                                                                                                                                                                                                                                                               ATTTGTTTTAGCTGGCAGTGCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACGGCTAAAGATTGACTTTGG 23
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                                                                                                              E: KNOBBE, MARTENS,
620 Newport Center
                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB
Pred. No. 1.9
0; Mismatches
                                                                                                               Drive
                                                                                                              OLSON AND BEAR
Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                        1.9e+03;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9e+03;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
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                                                                                                                             US-08-379-078-527
                                                            Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDN HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/974,406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                           Local Similarity nes 22; Conserv
                                                                                                                                                                                                         LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI:011CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                            147 AGCACCATTGTGAAACAGATGA 168
                                                              Conservative
                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                    Daniel !
                                                                                                                                                                            CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
In Release #1.0, Version #1.25
                                                           1.4%; Score 22; DB
100.0%; Pred. No. 3.
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/379,078
                                                                                                                                                                                                                                                                           527:
                                                                             DB 1; Le
                                                                                           Length 22
                                                              0
                                                           Gaps
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Search completed: September 14, 2004, 16:52:04 Job time : 145 secs

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24.2 1.6
         29 15 US-10-157-215A-204
        Sequence 204, App
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26.8 1.7 30 17 US-10-718-948-31 Sequence 31, Appl 25.8 1.7 29 17 US-10-718-948-33 Sequence 31, Appl 3 24.2 1.6 29 13 US-10-157-073-204 Sequence 204, Appl 4 24.2 1.6 29 13 US-10-157-1064-204 Sequence 204, Appl 5 24.2 1.6 29 13 US-10-157-171-204 Sequence 204, Appl 6 24.2 1.6 29 13 US-10-157-491-204 Sequence 204, Appl 7 24.2 1.6 29 13 US-10-157-92A-204 Sequence 204, Appl 8 24.2 1.6 29 13 US-10-157-178-204 Sequence 204, Appl 9 24.2 1.6 29 13 US-10-157-178-204 Sequence 204, Appl 10 24.2 1.6 29 13 US-10-157-178-204 Sequence 204, Appl 11 24.2 1.6 29 15 US-10-157-313-204 Sequence 204, Appl 12 24.2 1.6 29 15 US-10-157-305-204 Sequence 204, Appl 12 24.2 1.6 29 15 US-10-157-305-204 Sequence 204, Appl 13 24.2 1.6 29 15 US-10-157-305-204 Sequence 204, Appl 13 24.2 1.6 29 15 US-10-157-305-204 Sequence 204, Appl 14 24.2 1.6 29 15 US-10-157-305-204 Sequence 204, Appl 15 US-10-157-312-204 Sequence 204, Appl 16 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 17 25 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-312-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-313-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-313-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 204, Appl 18 24.2 1.6 29 15 US-10-157-315A-204 Sequence 2	16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:* 17: /cgn2_6/ptodata/1/pubpna/US10.NEW_PUB.seq:* 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result Ouery No. Score Match Length DB ID Description	Database: Published_Applications_NA:* 1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:* 2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:* 3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:* 4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:* 5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:* 6: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:* 7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:* 9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:* 9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:* 10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:* 11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:* 12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:* 13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:* 14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:* 14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	eq length: 0 eq length: 30	Searched: 3304383 seqs, 2515761380 residues Total number of hits satisfying chosen parameters: 1414684	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Title: US-10-018-497A-1 Perfect score: 1543 Sequence: 1 gaattcggatgggctgcacgtgaaaaaaaagccgaattc 1543	Run on: September 14, 2004, 14:03:51 ; Search time 761 Seconds (without alignments) 10201.892 Million cell updates/sec	OM nucleic - nucleic search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
; TYPE: DNA ; ORGANISM: Artificial Sequence ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: primer US-10-718-948-31 Query Match Best Local Similarity 93.3%; Pred. Matches 28; Conservative 0; Mis Matches 28; Conservative 0; Mis Oy 462 GCTTCATATTATCTAAATGATCTGGA	APPLICANT: Schreiner, George TITLE OF INVENTION: CHANGE IN THE BE FILE REFERENCE: 39739-0029 CURRENT APPLICATION NUMBER: US/10/718 CURRENT FILING DATE: 2003-11-20 PRIOR APPLICATION NUMBER: 60/429046 PRIOR FILING DATE: 2003-09-18 PRIOR APPLICATION NUMBER: 60/429046 PRIOR APPLICATION NUMBER: 60/429046 PRIOR FILING DATE: 2002-11-22 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 31	44 22 1.4 30 15 US-1 45 22 1.4 30 15 US-1 AI SULT 1 SULT 1 Sequence 31, Application US/10718948 Publication No. US20040127575A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Feng, Ying APPLICANT: Higgings, Linda APPLICANT: Kapoun, Ann	C 39 22 1.4 30 15 US-10- C 40 22 1.4 30 15 US-10- C 41 22 1.4 30 15 US-10- C 42 22 1.4 30 15 US-10- C 43 22 1.4 30 15 US-10-	36 22 1.4 30 15 US-1 37 22 1.4 30 15 US-1 38 22 1.4 30 15 US-1	33 22 1.4 30 13 US-1 34 22 1.4 30 13 US-1 35 22 1.4 30 15 US-1	30 22 1.4 30 13 US-1 31 22 1.4 30 13 US-1 32 27 1.4 30 13 US-1	26 24.2 1.6 29 16 US-1 27 23.2 1.5 28 17 US-1 28 22 1.4 30 13 US-1 29 22 1.4 30 13 US-1	24.2 1.6 29 16 US- 24.2 1.6 29 16 US- 24.2 1.6 29 16 US- 24.2 1.6 29 16 US- 24.2 1.6 29 16 US-	24.2 1.6 29 15 US-1 24.2 1.6 29 15 US-1 24.2 1.6 29 15 US-1	24.2 1.6 29 15 US-1 24.2 1.6 29 15 US-1 24.2 1.6 29 15 US-1 24.2 1.6 29 15 US-1

5	44	43	42	41	0	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15
22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	23.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2
1.4	1.4	1.4	•	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4			1.5		•			•		•	•	•	٠		
30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	28	29	29	29	29	29	29	29	29	29	29	29	29
15	15	<u>۲</u>	15	15	15	15	15	15	15	15	13	13	13	13	13	13	13	17	16	16	16	16	16	15	15	15	15	15	15	15
6-902-	-10-157-1	-10-157-147-	6-831-	-10-154-951E	0-157-2	-10-157	-10-157	-10-15	-10-157	-10-157	-10-157	-10-157	-10-156	US-10-157-491-205	-10-157	-10-157	-10-157-073-	œ	ᅩ	-10-157	-10-157-418A-	-10-157-320A-2	-10-156-811-	-10-157-	-10-156-902-	-10-157-166-	-10-	-10-156-831-	-10-154-9	US-10-157-299-204
Sequence 205, App	equence	205	205,	e 205,	e 205,	e 205,	e 205,	e 205,	205,	205,	205,	205,	205,	205,	205,	205,	205,	30,	204,	204,	204,	e 204,	204,	e 204,	e 204,	e 204,	e 204,	e 204,	e 204,	Sequence 204, App

ALIGNMENTS

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ATCTGGATAGA 491
|| |||||||
ATTTGGATAGA 30
                                               Score 26.8; DB 17; Length 30;
Pred. No. 5.2e+03;
D; Mismatches 2; Indels 0; Gaps
                                                                                                                                                                                                                                29046
                                                                                                                                                                                                                                                        )4585
                                                                                                                                                                                          ersion 4.0
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0
                                                                                                                                                                                                                                                                                                           COUNTERACTING A PATHOLOGIC THE BETA-ADRENERGIC PATHWAY
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RESULT 2 US-10-718-948-33

Sequence 33, Application US/107: Publication No. US20040127575A1 GENERAL INFORMATION:

Application US/10718948

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US-10-157-073-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-718-948-33
                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 204, A. Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.7%;
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 29
                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sabbadini ROGER A.
TITLE OF INVENTION: MINICELL BASED SELECTIVE ABSORPTION
FILE REFERENCE: MPEX.008DV24
CURRENT APPLICATION NUMBER: US/10/157,073
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2002-05-25
PRIOR APPLICATION NUMBER: 10/154,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/718,948
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/504585
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/429046
PRIOR APPLICATION NUMBER: 60/429046
PRIOR FILING DATE: 2002-11-22
                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY FILE REFERENCE: 39739-0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feng, Ying APPLICANT: Higgings,
                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Neil.
APPLICANT: Sabb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 TCCCAGTCTAACTACATTCCAACTCAGCA 523
                                            11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
GGGCTGCACCGTGAGCGCCGAGGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCCAGACCAACTACATTCCAACTCAGCA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schreiner, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kapoun, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10157073 
b. US20030211086A1 |
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Linda
                                                                                      Score 24.2; DB 13
Pred. No. 2.4e+04;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25.8; DB 1 Pred. No. 9.2e+03
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29
                                                                                                                                          DB 13;
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                                                                                                                                     Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 29;
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                                                                                           0
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                                                                                      Gaps
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APPLICANT: Surber, Mark W.
APPLICANT: Surber, Mark W.
APPLICANT: Surber, Mark W.
TITLE OF INVENTION: MINICELL-BASED DELIVERY AGENTS
FILE REFERENCE: MPEX.008DV5
CURRENT APPLICATION NUMBER: US/10/157,106A
CURRENT FILING DATE: 2020-05-28
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
PRIOR PRILING DATE: 2002-05-24
PRIOR PRILING DATE: 2002-05-25
PRIOR PRILING DATE: 2001-05-24
NUMBER: OF SEQ ID NOS: 258
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                     US-10-157-171-204
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/157,171
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
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LENGTH: 29
    Matches
                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 204,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Surber, APPLICANT: Neil E APPLICANT: Willia
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: MPEX.008DV18
                                                                                                                                 LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: William Gerhart
ITTLE OF INVENTION: REVERSE SCREENING AND TARGET
ITTLE OF INVENTION: IDENTIFICATION WITH MINICELLS
                                                                                   FEATURE:
OTHER INFORMATION: Cloning primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sabbadini, Roger A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Cloning primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V Match 1.6%; Score 24.2; DB 13; Local Similarity 89.7%; Pred. No. 2.4e+04;
                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
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5. US20030224369A1
  Conservative
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                     1.6%;
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                     Score 24.2; DB 13; Pred. No. 2.4e+04;
Mismatches
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11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39

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GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

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APPLICANT: Berkley, Neil

APPLICANT: Klepper, Robert

APPLICANT: Surber, Mark W.

TITLE OF INVENTION: METHODS OF MINICELL-BASED DELIVERY

FILE REFERENCE: MPEX.008DV6

CURRENT APPLICATION NUMBER: US/10/156,792A

CURRENT FILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: 10/154,951

PRIOR FILING DATE: 2002-05-24

PRIOR FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/359,843

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
CRCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cloning primer
US-10-157-491-204
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US-10-156-792A-204
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CURRENT APPLICATION NUMBER: US/10/157,491

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION UNMBER: 60/293,566

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 60/359,843

PRIOR FILING DATE: 2002-02-25

PRIOR APPLICATION NUMBER: 10/154,951

PRIOR APPLICATION NUMBER: 10/154,951

PRIOR FILING DATE: 2002-05-24
                                                                   ; OTHER INFORMATION: Cloning primer US-10-156-792A-204
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                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sabbadini, Roger A.
APPLICANT: Berkley, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 204, Application US/10156792A Publication No. US20030203411A1
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Query Match
Best Local Similarity
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APPLICANT: Neil Berkley
APPLICANT: Mark W. Surber
TITLE OF INVENTION: MEMBRANE PROTEINS
TITLE OF INVENTION: MEMBRANE PROTEINS
                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/293,566
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                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                TYPE: DNA
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1.6%;
89.7%;
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Pred. No. 2.4e+04;
Score 24.2; DB 13;
Pred. No. 2.4e+04;
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CURRENT APPLICATION NUMBER: US/10/157,213
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR PRIOR DATE: 2001-05-24
PRIOR PRIOR DATE: 2002-02-25
PRIOR PRIOR PAPLICATION NUMBER: 10/154,951
PRIOR PRIOR PRIOR DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
TYPE: DNA
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PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/259,843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
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US-10-157-178-204
                                                        ; OTHER INFORMATION: Cloning primer US-10-157-213-204
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; OTHER INFORMATION: Cloning primer US-10-157-178-204
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Publication No. US20030203481A1
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Klepper, Robert TITLE OF INVENTION: CONJUGATED MINICELLS FILE REFERENCE: MPEX.008DV7
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Surber, Mark W. APPLICANT: Klepper, Rober
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sabbadini, Roger A.
APPLICANT: Robert Klepper
APPLICANT: Neil Berkley
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CURRENT FILING DATE: 2002-08-29
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                            ORGANISM: Artificial Sequence FEATURE:
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LTLE OF INVENTION: MINICELL-BASED DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
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89.7%;
1.6%;
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Score 24.2; DB 13;
Pred. No. 2.4e+04;
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APPLICANT: Sabbadini, Roger A.
APPLICANT: Neil Berkley
TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
FILE REFERENCE: MPEX.008DV14
CURRENT APPLICATION NUMBER: US/10/157,391
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/29,566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
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US-10-157-391-204
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CURRENT APPLICATION NUMBER: US/10/157,305A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 204 LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 258
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
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                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Robert Klepper
TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equence 204, inblication No.
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OTHER INFORMATION: Cloning primer
                       ORGANISM: Artificial Sequence FEATURE:
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                                                                 TYPE: DNA
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Neil Berkley
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o. US20030166279A1 |
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Pred. No. 2.4e+04;
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Best Local S
Matches 26
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LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sabbadini, Roger A. APPLICANT: Surber, Mark W.
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TYPE: DNA
                   ORGANISM: Artificial Sequence FEATURE:
                                                              TYPE: DNA
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                                                                              ENGTH:
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; OTHER INFORMATION: Cloning primer US-10-157-302-204
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; OTHER INFORMATION: Cloning primer
US-10-157-096-204
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APPLICANT: Surber, Mark W.
APPLICANT: Surber, Mark W.
TITLE OF INVENTION: TARGET DISPLAY ON MINICELLS
FILE REFERENCE: MPEX.008DV12
CURRENT APPLICATION NUMBER: US/10/157,096
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR PILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 204, Application US/10157302 Publication No. US20030190683A1
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                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Surber, Mark W.

TITLE OF INVENTION: MINICELL-BASED RATIONAL DRUG DESIGN
FILE REFERENCE: MPEX.008DV17

CURRENT APPLICATION NUMBER: US/10/157,302

CURRENT FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 10/154,51
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/293,566 PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
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Similarity 89.7%; Pred. No. 2.4e+04;
26; Conservative 0; Mismatches 3;
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APPLICANT: Neil Berkley
APPLICANT: Neil Berkley
APPLICANT: Neil Berkley
APPLICANT: Surber, Mark W.
APPLICANT: Surber, Mark W.
FILE REFERENCE: MPEX.008DV15
CURRENT APPLICATION WIMPER: US/10/157,299
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION WUMBER: 60/293,566
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTMARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
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ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-1.0-157-215A-204
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US-10-157-215A-204
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/157,215A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-05-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR ETILING DATE: 2002-05-25
PRIOR APPLICATION NUMBER: 10/154,951
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APPLICANT: Berkley, Neil
TITLE OF INVENTION: MINICELL-PRODUCING PARENT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Surber, Mark W.
APPLICANT: Sabbadini, Roger A.
ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Cloning primer
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Pred. No. 2.4e+04;
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D18738 MUSGS01800
CF305384 CLD1--01D11538 HUMOCL2B03BQ584385 E011858-0
BZ358395 SALK 1324
AZ462631 1M0269F12
AZ581086 1M0369F11
CC20896 HUMGS000497
CF319624 HD--10-D0
AV739265 AV739265
AZ27011 2M0103112
AU257497 AU257497
AU257497 AU257497
AU267300 AU267300
CC00680 HUMGS000823
AZ773045 1M058A10
AZ444586 1M0236M13
AZ344757 1M008A10
AZ444586 1M0236M13
AU246784 2822003
AZ19217 HUM000S318
AW059699 AHUTH.D88
D12217 HUM000S318
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D12217 HUM000S318
AW059699 AHUTH.D88
D12304 HUM000S318
AW059699 AHUTH.D88
D1231462 HUM00TW469
D12462 HUM00TW469
D12462 HUM00TW469
AZ43903 1M0220G03
AL048890 DKFZP566D
AZ581194 1M037708
AZ58127 1M0367108
AZ824122 2M0098M01
AZ579541 1M0367108
AZ286533 2M0068H09
AW248759 2820825.3
D18724 MUSGS01786
AZ246533 2M0066H124
AZ25569 1M04651124
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Maximum Match
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Maximum DB seq length: 30
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12333.336 Million cell updates/sec
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  AL480654 T. brucei
AZ650939 1M0521D19
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                                                       Description
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TA224C08P/c
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ORGANISM
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KEYWORDS
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                                                                                                     TITLE
JOURNAL
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Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucel (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small
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T. brucei sheared genomic DNA
genomic survey sequence.
AL1480654
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Trypanosoma brucei
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B AZ581086
C20896
CC20896
AV7392624
AV7392627011
AV2527012
AV267309
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AZ442586
AD12217
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CF305384
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A clone
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linear

forward sequence,

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AZ650939/c
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Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0521 row: D column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi, Muridae; Musinae; Mus. 1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0521D19F Mouse 10kb clone UUGC1M0521D19 F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 30.
Location/Qualifiers
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                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector:| PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jaboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNI was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0521D19"
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|mol_type="genomic DNA"
|strain="TREU927"
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/clone="224c08"
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RESULT 3
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Matches 23; Conserv
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbbo.com, bhna
Location/Qualifiers
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Genomics and Genetics Institute,
of Bloscience and Bloinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large-scale Sequencing Analysis 
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="CLD1--01-B13"
/tissue_type="leaf"
                                                                                                                                                                                            /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C(360uM/m-28ec-\overline{1}) for 2hrs. Oligo-campanas reverse transcribed and then used for PCR.
                                                                                                                                                                                                                                                                       /dev_stage="14 days after germination"
/lab_host="B.coli DH10B"
/clone lib="Rice cold treated leaf plasmid cDNA library
/crn11"
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; Pred. No. 3.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bhnahm@bio.myongji.ac.kr
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SOURCE

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Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
                                                                                                                            cDNA sequencing Unpublished (1995) Contact: Kawamoto,S.,
                                                                                                                                                                       Mus musculus domesticus (western European house mouse)
Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 26)
1 (bases 1 to 26)
Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3'-directed
                                                                                                                                                                                                                                                                                         D18738.1 GI:1100707
EST.
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MUSGS01800 Mouse 3'-directed
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University of Tsukuba
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1 (bases 1 to 30)
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                                                                                                              Matsubara, K.
                                                                                                 Institute for Cellular and Molecular Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hideko@biol.tsukuba.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
/organism="Mus musculus domesticus"
/mol_type="mRNA"
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:44689"
/clone="VSD485"
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                           mRNA
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                                                                                                                                                                                                                                                                                                                                                          linear EST 12-DEC-1995
domesticus cDNA clone
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LOCUS DEFINITION RESULT 7 D11538/c

D11538 25 bp HUMOC12B03 Liver HepG2 cell line.

Нопо

mRNA

A linear EST 02-DEC-1992 sapiens cDNA clone c12b03,

mRNA sequence.

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JOURNAL COMMENT
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AUTHORS
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CF305384
LOCUS
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ORGANISM
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Best Local S
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CLD1--01-J01.b1 Rice cold treated leaf
Cryza sativa cDNA clone CLD1--01-J01, m
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics and Genetics Institute, of Bioscience and Bioinformatics, Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF305384.1
                                                                                                                                                                                                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
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 TTTTTGGGAAAAAAAAAAAAAAAAGGCG
                       TTTTTGAGGAAAAAATAAAGAGGAG 850
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                                                                  Conservative
                                                                                                                                                  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C(360uM/m-2sec-I) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sub_species="domesticus"
/db_xref="taxon:10092"
/clone="md1688"
                                                                                                                                                                                                                                    /db_xref="taxon:4530"
/clone="CLD1--01-J01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli_DH10B"
                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_lib="Mouse 3'-directed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                        'clone lib="Rice cold treated leaf plasmid cDNA library
(CLD1)"
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Pred. No. 4.2e+07;
0; Mismatches 5
                                                                Score 17; DB 14;
Pred. No. 4.2e+07;
0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                              bhnahm@bio.myongji.ac.kr
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, MyongJi University
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                                                                                                                                                 COMMENT
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D11538.1
EST.
                                                                                                                                                                                                                                                         Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath, Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQ584385 26 bp mRNA linear E011858-024-003-A19-SP6 MPIZ-ADIS-024-inflorescence CDNA clone 024-003-A19 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kousaku Okubo, Naohiro Hori, Ryo Ma
Niiyama, Atsushi Fukushima, Yuko Kojima & Ke
Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large scale cDNA sequencing for analysis of qualitative aspects of gene expression Nat. Genet. 2, 173-179 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 25)
Okubo,K., Hori,N., Matoba,R., Niiyama,T.,
and Matsubara,K.
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 26 Std!Error: 0.00
Plate: 3 row: A column: 19
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet great J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantaė; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          Contact: Weisshaar B
ADIS DNA core facility at MPIZ
                                                                                                                                                                                                                                                                                                                                                                                    Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ584385.1 GI:26113962
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                                                                                        Carl-von-Linne Weg 10, 50829
                                                                                                             Max-Planck-Institute
                                                                                                                                                                  12472698
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                                                                           Fax:-00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTTTATAACTTTATTTG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Liver HepG2 cell line."
/note="3'-directed regional cDNA library.
and transformed into E.coli."
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Pred. No. 4
                                                                                                             Plant Breeding Research
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Kenichi
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Matsubara
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BZ358395.1
GSS.
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                                                                                                                                                                                                                                                                                                        Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H. Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BZ358395 27 bp DNA linear GSS SALK 132488.23.30.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 132488.23.30.x,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                   Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            survey sequence.
                                                                                                                                                                                                                                                                This is single pass sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                     ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
bs:chulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinaters of Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Sequencing granted in the context of the GABI-Beet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
/db_xref="taxon:3702"
/clone="SALK_132488.23.30.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
                                                                                                   /mol_type="genomic I
/strain="Columbia 0"
                                                                                                                                              organism="Arabidopsis
                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="024-003-A19"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:24950657
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0; Mismatches
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                                                                                                                                                thaliana"
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Best Local &
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: F column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 20.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi]4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                       musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC1M0269F12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                       sex="Male"
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Pred. No. 5.2e+07;
0; Mismatches 4
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UUGC1M library Mus musculus genomic
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AZ581086/c
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1M0369E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0369E11 R, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: E column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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801 585 7177
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The bheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-" (clone lib="Mouse 10kb plasmid UUGCIM library" (note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jacksor Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                       sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                  clone="UUGC1M0369E11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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[7]
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RESULT 13
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C20896/c
                                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1364 GCATTCTAGAACTTCATATGTAGCTT 1389
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                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               We are not submitting the same CDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute for Molecular and Cellular Biol Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C20896
30 bp mRNA linear EST 31-DEC-2002
HUMGS0004970 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
                                                                                            HD--10-D06.b1 OsHDAC1-overexpressing transgenic rice plasmid collibrary (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
Contact: Okubo, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okubo, K.
BodyMap; human gene expression database
                                                        CF319624.1 GI:33691385
                                                                          library (HD)
CF319624
                                                                                                                                   CF319624
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Pred. No. 5.6e
0; Mismatches
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AV739265/c
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1 (bases 1 to 30)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                    Contact: Zhu Chen
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin
Shanghai 200025, P. F
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 27)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     v
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Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                 Chinese National Human Genome Center at Sha
351 Guo Shoujing Road, Zhangjiang Hi- Tech
Location/Qualifiers
                                                                                                                                                      Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                       197 Rui-Jin II Road,
Tel: 86-21-64740490
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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AV739265
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV739265.1 GI:10856846
                                                                                                                                                                                                   Fax: 86-21-64743206
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="HD--10-D06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stāge="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="callus"
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'mol type="mRNA"
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A clone CBFAWE01 5',
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clone="CBFAWE01" db_xref="taxon:9606"

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AZ827011/c
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error:
Plate: 0103 row: I column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ827011.1 GI:12996919 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript; Site 1: EcoRI; cloned randomly with the EcoRI digestion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                   clone="UUGC2M0103I12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.2; DB 9;
Pred. No. 6.3e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UUGCIM library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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COMMENT

electrophoresis. Vector DNA was prepared from a derivative of pWn42 (gi|4732114|gb|AFI19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Ś Matches Query Match Best Local Similarity 21; Conservative 1.0%; Score 16.2; DB 28 Pred. No. 6.2e+07; 0; Mismatches 8 28; Length Indels 29; 0 Gaps

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SOURCE

Search completed: September 14, 2004, 16:49:28 Job time: 3741 secs